Amendments to the Specification:

Please replace the paragraph at page 20, from line 1 through line 7, with the following paragraph:

--   Identity is often measured using sequence analysis software *e.g.*, BLASTN or BLASTP (available at the world wide web site ("www") for the National Center for Biotechnology Information (".ncbi") of the National Institutes of Health (".nih") of the U.S. government (".gov"), in the "/BLAST/" directory [http://www.ncbi.nlm.nih.gov/BLAST/]). The default parameters for comparing two sequences (*e.g.*, "Blast"-ing two sequences against each other[, http://www.ncbi.nlm.nih.gov/gorf/bl2.html]) by BLASTN (for nucleotide sequences) are reward for match = 1, penalty for mismatch = -2, open gap = 5, extension gap = 2. When using BLASTP for protein sequences, the default parameters are reward for match = 0, penalty for mismatch = 0, open gap = 11, and extension gap = 1. --